

#4

SEQUENCE LISTING

<110> Katherine Galvin and Laura A. Rudolph-Owen

<120> METHODS AND COMPOSITIONS FOR THE DIAGNOSIS
AND TREATMENT OF CARDIOVASCULAR AND TUMORIGENIC
DISEASE USING 4941

<130> MNI-094

<140> 09/635,521

<141> 2000-08-09

<150> 60/199,908

<151> 2000-04-26

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1359)

<400> 1

atg gct tca ccc agc ctc ccg ggc agt gac tgc tcc caa atc att gat	48
Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp	
1 5 10 15	
cac agt cat gtc ccc gag ttt gag gtg gcc acc tgg atc aaa atc acc	96
His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr	
20 25 30	
ctt att ctg gtg tac ctg atc atc ttc gtg atg ggc ctt ctg ggg aac	144
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn	
35 40 45	
agc gcc acc att cgg gtc acc cag gtg ctg cag aag aaa gga tac ttg	192
Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu	
50 55 60	
cag aag gag gtg aca gac cac atg gtg agt ttg gct tgc tcg gac atc	240
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile	
65 70 75 80	
ttg gtg ttc ctc atc ggc atg ccc atg gag ttc tac agc atc atc tgg	288
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp	
85 90 95	
aat ccc ctg acc acg tcc agc tac acc ctg tcc tgc aag ctg cac act	336
Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr	
100 105 110	



ttc ctc ttc gag gcc tgc agc tac gct acg ctg ctg cac gtg ctg aca	384
Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr	
115 120 125	
ctc agc ttt gag cgc tac atc gcc atc tgt cac ccc ttc agg tac aag	432
Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys	
130 135 140	
gct gtg tcg gga cct tgc cag gtg aag ctg ctg att ggc ttc gtc tgg	480
Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp	
145 150 155 160	
gtc acc tcc gcc ctg gtg gca ctg ccc ttg ctg ttt gcc atg ggt act	528
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr	
165 170 175	
gag tac ccc ctg gtg aac gtg ccc agc cac cgg ggt ctc act tgc aac	576
Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn	
180 185 190	
cgc tcc agc acc cgc cac cac gag cag ccc gag acc tcc aat atg tcc	624
Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser	
195 200 205	
atc tgt acc aac ctc tcc agc cgc tgg acc gtg ttc cag tcc agc atc	672
Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile	
210 215 220	
ttc ggc gcc ttc gtg gtc tac ctc gtg gtc ctg ctc tcc gta gcc ttc	720
Phe Gly Ala Phe Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe	
225 230 235 240	
atg tgc tgg aac atg atg cag gtg ctc atg aaa agc cag aag ggc tcg	768
Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser	
245 250 255	
ctg gcc ggg ggc acg cgg cct ccg cag ctg agg aag tcc gag agc gaa	816
Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu	
260 265 270	
gag agc agg acc gcc agg agg cag acc atc atc ttc ctg agg ctg att	864
Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile	
275 280 285	
gtt gtg aca ttg gcc gta tgc tgg atg ccc aac cag att cgg agg atc	912
Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile	
290 295 300	
atg gct gcg gcc aaa ccc aag cac gac tgg acg agg tcc tac ttc cgg	960
Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg	
305 310 315 320	
gcg tac atg atc ctc ctc ccc ttc tcg gag acg ttt ttc tac ctc agc	1008
Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser	
325 330 335	

tcg gtc atc aac ccg ctc ctg tac acg gtg tcc tcg cag cag ttt cgg	1056
Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg	
340 345 350	
cgg gtg ttc gtg cag gtg ctg tgc tgc cgc ctg tcg ctg cag cac gcc	1104
Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala	
355 360 365	
aac cac gag aag cgc ctg cgc gta cat gcg cac tcc acc acc gac agc	1152
Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser	
370 375 380	
gcc cgc ttt gtg cag cgc ccg ttg ctc ttc gcg tcc cgg cgc cag tcc	1200
Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser	
385 390 395 400	
tct gca agg aga act gag aag att ttc tta agc act ttt cag agc gag	1248
Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu	
405 410 415	
gcc gag ccc cag tct aag tcc cag tca ttg agt ctc gag tca cta gag	1296
Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu	
420 425 430	
ccc aac tca ggc gcg aaa cca gcc aat tct gct gca gag aat ggt ttt	1344
Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe	
435 440 445	
cag gag cat gaa gtt tga	1362
Gln Glu His Glu Val	
450	

<210> 2
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 2	
Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp	
1 5 10 15	
His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr	
20 25 30	
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn	
35 40 45	
Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu	
50 55 60	
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile	
65 70 75 80	
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp	
85 90 95	

Asn	Pro	Leu	Thr	Thr	Ser	Ser	Tyr	Thr	Leu	Ser	Cys	Lys	Leu	His	Thr	100	105	110
Phe	Leu	Phe	Glu	Ala	Cys	Ser	Tyr	Ala	Thr	Leu	Leu	His	Val	Leu	Thr	115	120	125
Leu	Ser	Phe	Glu	Arg	Tyr	Ile	Ala	Ile	Cys	His	Pro	Phe	Arg	Tyr	Lys	130	135	140
Ala	Val	Ser	Gly	Pro	Cys	Gln	Val	Lys	Leu	Leu	Ile	Gly	Phe	Val	Trp	145	150	155
Val	Thr	Ser	Ala	Leu	Val	Ala	Leu	Pro	Leu	Leu	Phe	Ala	Met	Gly	Thr	165	170	175
Glu	Tyr	Pro	Leu	Val	Asn	Val	Pro	Ser	His	Arg	Gly	Leu	Thr	Cys	Asn	180	185	190
Arg	Ser	Ser	Thr	Arg	His	His	Glu	Gln	Pro	Glu	Thr	Ser	Asn	Met	Ser	195	200	205
Ile	Cys	Thr	Asn	Leu	Ser	Ser	Arg	Trp	Thr	Val	Phe	Gln	Ser	Ser	Ile	210	215	220
Phe	Gly	Ala	Phe	Val	Val	Tyr	Leu	Val	Val	Leu	Leu	Ser	Val	Ala	Phe	225	230	235
Met	Cys	Trp	Asn	Met	Met	Gln	Val	Leu	Met	Lys	Ser	Gln	Lys	Gly	Ser	245	250	255
Leu	Ala	Gly	Gly	Thr	Arg	Pro	Pro	Gln	Leu	Arg	Lys	Ser	Glu	Ser	Glu	260	265	270
Glu	Ser	Arg	Thr	Ala	Arg	Arg	Gln	Thr	Ile	Ile	Phe	Leu	Arg	Leu	Ile	275	280	285
Val	Val	Thr	Leu	Ala	Val	Cys	Trp	Met	Pro	Asn	Gln	Ile	Arg	Arg	Ile	290	295	300
Met	Ala	Ala	Ala	Lys	Pro	Lys	His	Asp	Trp	Thr	Arg	Ser	Tyr	Phe	Arg	305	310	315
Ala	Tyr	Met	Ile	Leu	Leu	Pro	Phe	Ser	Glu	Thr	Phe	Phe	Tyr	Leu	Ser	325	330	335
Ser	Val	Ile	Asn	Pro	Leu	Leu	Tyr	Thr	Val	Ser	Ser	Gln	Gln	Phe	Arg	340	345	350
Arg	Val	Phe	Val	Gln	Val	Leu	Cys	Cys	Arg	Leu	Ser	Leu	Gln	His	Ala	355	360	365
Asn	His	Glu	Lys	Arg	Leu	Arg	Val	His	Ala	His	Ser	Thr	Thr	Asp	Ser	370	375	380
Ala	Arg	Phe	Val	Gln	Arg	Pro	Leu	Leu	Phe	Ala	Ser	Arg	Arg	Gln	Ser	385	390	395

Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
405 410 415

Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
420 425 430

Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
435 440 445

Gln Glu His Glu Val
450

<210> 3
<211> 2528
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (42)..(1400)

<220>
<223> N at positions 2490 and 2493 may be Adenine,
Guanine, Cytosine or Thymine

<400> 3
gggagtcgac ccacgcgtcc ggtagcctgg tgctctttct c atg gct tca ccc agc 56
Met Ala Ser Pro Ser
1 5

ctc ccg ggc agt gac tgc tcc caa atc att gat cac agt cat gtc ccc 104
Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp His Ser His Val Pro
10 15 20

gag ttt gag gtg gcc acc tgg atc aaa atc acc ctt att ctg gtg tac 152
Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr Leu Ile Leu Val Tyr
25 30 35

ctg atc atc ttc gtg atg ggc ctt ctg ggg aac agc gcc acc att cgg 200
Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn Ser Ala Thr Ile Arg
40 45 50

gtc acc cag gtg ctg cag aag aaa gga tac ttg cag aag gag gtg aca 248
Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu Gln Lys Glu Val Thr
55 60 65

gac cac atg gtg agt ttg gct tgc tgc gac atc ttg gtg ttc ctc atc 296
Asp His Met Val Ser Leu Ala Cys Ser Asp Ile Leu Val Phe Leu Ile
70 75 80 85

ggc atg ccc atg gag ttc tac agc atc atc tgg aat ccc ctg acc acg 344
Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp Asn Pro Leu Thr Thr
90 95 100

tcc agc tac acc ctg tcc tgc aag ctg cac act ttc ctc ttc gag gcc 392
Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr Phe Leu Phe Glu Ala

105

110

115

tgc agc tac gct acg ctg ctg cac gtg ctg aca ctc agc ttt gag cgc Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr Leu Ser Phe Glu Arg 120 125 130	440
tac atc gcc atc tgt cac ccc ttc agg tac aag gct gtg tcg gga cct Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys Ala Val Ser Gly Pro 135 140 145	488
tgc cag gtg aag ctg ctg att ggc ttc gtc tgg gtc acc tcc gcc ctg Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp Val Thr Ser Ala Leu 150 155 160 165	536
gtg gca ctg ccc ttg ctg ttt gcc atg ggt act gag tac ccc ctg gtg Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr Glu Tyr Pro Leu Val 170 175 180	584
aac gtg ccc agc cac cgg ggt ctc act tgc aac cgc tcc agc acc cgc Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn Arg Ser Ser Thr Arg 185 190 195	632
cac cac gag cag ccc gag acc tcc aat atg tcc atc tgt acc aac ctc His His Glu Gln Pro Glu Thr Ser Asn Met Ser Ile Cys Thr Asn Leu 200 205 210	680
tcc agc cgc tgg acc gtg ttc cag tcc agc atc ttc ggc gcc ttc gtg Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile Phe Gly Ala Phe Val 215 220 225	728
gtc tac ctc gtg gtc ctg ctc tcc gta gcc ttc atg tgc tgg aac atg Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe Met Cys Trp Asn Met 230 235 240 245	776
atg cag gtg ctc atg aaa agc cag aag ggc tgc ctg gcc ggg ggc acg Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser Leu Ala Gly Gly Thr 250 255 260	824
cgg cct ccg cag ctg agg aag tcc gag agc gaa gag agc agg acc gcc Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu Glu Ser Arg Thr Ala 265 270 275	872
agg agg cag acc atc atc ttc ctg agg ctg att gtt gtg aca ttg gcc Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile Val Val Thr Leu Ala 280 285 290	920
gta tgc tgg atg ccc aac cag att cgg agg atc atg gct gcg gcc aaa Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile Met Ala Ala Ala Lys 295 300 305	968
ccc aag cac gac tgg acg agg tcc tac ttc cgg gcg tac atg atc ctc Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg Ala Tyr Met Ile Leu 310 315 320 325	1016
ctc ccc ttc tcg gag acg ttt ttc tac ctc agc tcg gtc atc aac ccg Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser Ser Val Ile Asn Pro 330 335 340	1064

ctc ctg tac acg gtg tcc tcg cag cag ttt cgg cgg gtg ttc gtg cag	1112
Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg Arg Val Phe Val Gln	
345 350 355	
gtg ctg tgc tgc cgc ctg tcg ctg cag cac gcc aac cac gag aag cgc	1160
Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala Asn His Glu Lys Arg	
360 365 370	
ctg cgc gta cat gcg cac tcc acc acc gac agc gcc cgc ttt gtg cag	1208
Leu Arg Val His Ala His Ser Thr Thr Asp Ser Ala Arg Phe Val Gln	
375 380 385	
cgc ccg ttg ctc ttc gcg tcc cgg cgc cag tcc tct gca agg aga act	1256
Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser Ser Ala Arg Arg Thr	
390 395 400 405	
gag aag att ttc tta agc act ttt cag agc gag gcc gag ccc cag tct	1304
Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu Ala Glu Pro Gln Ser	
410 415 420	
aag tcc cag tca ttg agt ctc gag tca cta gag ccc aac tca ggc gcg	1352
Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu Pro Asn Ser Gly Ala	
425 430 435	
aaa cca gcc aat tct gct gca gag aat ggt ttt cag gag cat gaa gtt	1400
Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe Gln Glu His Glu Val	
440 445 450	
tgaatgtcaa gcgagggagc cttgagtggg aactggccct ccagccctaa gaaaacgtca	1460
ctctcactct gcagtctcaa actatgcccc catcagggat ggaatggaca ctggaggctt	1520
tacaaaaggc agatgccac ctcatgtact tctaaggact gactctgcca gcctggcctt	1580
gactccggtt acacagacat ggggggtgaac tttcactcca cctccttcct tcaagtacat	1640
actgaaaatt cagtcaagct gaatttattc agaatgcttt accgagctct ttcattattt	1700
gcacaggaac aaaagagaac acggactccc gtccttacc cagaataaaa ggacaccag	1760
aagaaactca ctgaggagg tgggggggttg ggggcgagg ctggaagaac aatgcaggag	1820
ggggtggcat ctcttcagc ttcagcagt tgccgagaag agggctaatt tgaggaacag	1880
gatggtggtg cggagccctg gcctgagggc cgaggcagaa cttcccttt tcttgggcct	1940
tggcccggtta caaagagggg tgttgcagca gctgatgcaa actgagttca gtttccttg	2000
ggagcagaag gactggtacc cggcagaggc gatgagacag gccgctgatg atgcacagga	2060
cttgcggtac atgatcccg cactttgctc catcattct ttctgacaca tgtcttgaac	2120
gttcaccgtg caattcaca tgaactcggg ggaggagcag tcgttggtca gctggaattc	2180
ttcacactgg tagcactgga tttgcagcgc aaagccttgc ggactcccg ggatgccccg	2240

gtgctatctt cgccttcctt cccgagcctt gcagcaggtg gtgcgggaga ccgcttgccc 2300
gccggagtgc gttggtgccc ccgcccccaa tccgcacatt cccatcccct ttccgcacat 2360
ccttagggag catccatttc cgtggaaatc gcctcctaag ctttagctcc tcttcaccct 2420
tttctcccc gcccaattct gggggcagct ctctcacgcc gggacgcaga tcatttaatt 2480
ctgcatcgcn tcngcagagc tggctctgtaa aggggcttaa atgacttt 2528